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RESULT 2
I62749
LOCUS       I62749         5200 bp    DNA      linear   PAT 07-OCT-1997.
DEFINITION  Sequence 12 from patent US 5660982.
ACCESSION   I62749
VERSION     I62749.1  GI:2480457
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 5200)
  AUTHORS   Tryggvason,K.; Kallunki,P.; and Pyke,C.
  TITLE     Laminin chains: diagnostic uses
  JOURNAL   Patent: US 5660982-A 12 26-AUG-1997;
FEATURES             Location/Qualifiers
     source          1..5200
                     /organism="unknown"
BASE COUNT     1364 a   1236 c   1392 g   1208 t
ORIGIN

Query Match       74.9%;  Score 2986.2;  DB 6;  Length 5200;
Best Local Similarity  88.5%;  Pred. No. 0;
Matches 3328;  Conservative 0;  Mismatches 403;  Indels 30;  Gaps 7;
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Qy     99 AAGGAAAAAGGAGGAGCACAGAGGAGGCGGAGCCGAGAGTGAGAACTCCCAGTGGGGGAGGCGGCCCGGC 158
          |||||||||||||||||||||||||||||||||||||||||||||||    |||||||||||
Db     14 AAGGAAAAAGGAAGGCACAGCGGAGGCGGAGAGCACCAAC--CGAGGCGCCGGGGC 71

Qy    159 AGGGGACCCCCTGCAGCGGGCG------GACCGCGGCCGGGCCGCCTGGCGCTGGCGCTCTG 211
          |||||||||||||||||||         ||||||||||||||||||||||||||||||
Db     72 AGCGACCCCCTGCAGCGGGAGACAGAGACTGAGGCGCGCACCGCCCATGCCTGCTGGCGCTCTG 131

Qy    212 GCTGAGCTGCTACCTCCTGCTTCTCGCCTTCTCCTCCTGCGCCCAGCCCGCCCGGGGCCACCTCCCGGGAG 271
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    132 GCTGGGCCTCGCTGCCTTCTCCGCCTTCTCCCTGCGCCGGGCCGCCACCTCCAGGAG 191

Qy    212 ...
          ...
Db    192 GGAAGTCTGTGATTGCAACGGGAGTCCAGCCAATGCATTCTTTGACCCAGGAACTTCACAA 251

Qy    272 GGAAGTCTGTGATTGCAACGGGAGTCCAGCCAATGCATTCTTTGACCCAGGAACTTCACAA 331
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    252 ACAAACTGGTAATGGATTCCGCTGCTCAACTGACAACACTGATGGGATGGGCATTCACTG 311

Qy    332 ACAGACAGGAAATGGATTCCGCTGCTCAACTGACAACACTGATGGGATGGGCATTCACTG 391
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    312 CGAGAAGTGCAAGAAATGGCTTTTACCGGACAACAGAGAAAGGGACGCTGTTTGCCCTGCAA 371

Qy    392 CGAGAGGTGCAAGGCAGAGCAGGATTTTACCCGACAGAGAGAAGAAGGGACGCTGTTTGCCCTGCAA 451
          |||||||||||||||||||||||||||||||||||||||
Db    372 TTGTAACTCCAAAGGTTCTCCTTAGTGCTCAGTGACACGTTGACCCAGCTGG 431

Qy    452 TTGTAAACTCTAAAGGTTCTTCTTAGGCTCGGATTGTACAACAACTCTGGACGGTGCAGCTGTAA 511
          |||||||||||||||||||||||||||||||||||||
Db    432 ACCAGCTGTGACAGGAGCCAGATGCTGCCCAGGCTTCCAGAGCTCACGGA 491

Qy    512 GCCAGGTGTGACAGGACAGCAGGTGTGACCGGATGCCGATGGTCTGCGCCGGCTTCCACACTCACTGA 571
          |||||||||||||||||||||||||||||
Db    492 TGCCTGGGTGCGCGCCCAAAGACCCAAAAGGCTCACGGGCCTTGTGACTGGAGAGCG 551

Qy    572 TGCTCGGGTGCGCGCCCAAGACCAAAGGCTGCTAGACTCCACAGTGTCTGCAAGACTCCAAGTGTGAACTG 631
          |||||||||||||||||||||||||||||||||||||
Db    552 CATCTCAGGGCCTGTGACTCAGGCCGTGCCTGTCGAGGCCCGTGTCACTGGATGCACAAG 611

Qy    632 CATCTCAGGGCCCTGTGACTGGAGCCGGGGCGCCGGCTTGTCAAGCACCAGCTGTTACTGGAGAACG 691
          |||||||||||||||||||||||||||||||||||||
Db    612 CTGTGATAGGTGTCGATCAGGTTACTAATAATCGGATGGGGGAAACCCTGGGGAAGCGCTAC 671

Qy    692 CTGTGATAGGTGTCGGACAGGTTACTATCACCTGGAATGGGGGAAACCCTGGGGAAGCCCTGGCTCC 751
          |||||||||||||||||||||||||||||||||||||
Db    672 CCAGTGTTTTGCTATAGGGGCCATTCCGCACGCTCGCCAGCTGACAGCTGACAGCTGTGTTCCA 731

Qy    752 CCAGTGTTTTGCTATAGGGGCCATTCCGCACGCTCGCCAGCTGACAGCTGACAGCTGTGTTCCA 811
          |||||||||||||||||||||||||||||||||||||
Db    812 TAAAATCATCCTGCCTTCCATCAAGATGTTGATGGCTGGCCGGGCCAGCTTCTGCAGAAATACAGTGTCCA 871
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Db    732 TAAGATCACCTTCACCTTTCATCAAGATGTTGATGGCTGGCCAGGTTGCCAACG 791
          |||||||||||||||||||||||||||||||||||
Qy    872 GTCTCCTTGCCAAAAGCTCCAGTGGTCACAGCGGCCATCGGGATATATTTAGCTCAGCGACACG 931

Db    792 GTCTCCTTGCCAAAAGCTCCAATGGTCACAGCGGCCATCAAGATGTTTAGCTCAGCCCAACG 851
          |||||||||||||||||||||||||||||||||||
Qy    932 ATCAGACCCTGTCTATTTTGTTAGCTCCTGCCCAAATTTCTTGGGAATCAACAGGTGAGCTA 991

Db    852 ACTAGATCCTGTCTTATTTTTGTGGCCTCCTGCCAAATTTCTTGGGAATCAACAGGTGAGCTA 911
          |||||||||||||||||||||||||||||||||||
Qy    992 CGGGCAAAGCCCTATCTTTTTGACTACCCGTGGGATGGGATAGGGGGAGGGGCAGCAGAACA 1051

Db    912 TGGGCAAAGCCTGCTCCTTTGACTACCCGTGGGACAGCAGGAGGGCAGCAGAACACCCATCTGCCCA 971
          |||||||||||||||||||||||||||||||||||
Qy   1052 TGACGTGATCCTGGAAAGGTGCTGCTACCGGTCTCACGGATCACACAGCTCCCTTGAGCAA 1111

Db    972 TGATGTGATCCTGGAAGGTGCTGGTGTCTACCGGATCACAGCTCCCTTGAGATGGCCAA 1031
          |||||||||||||||||||||||||||||||||||
Qy   1112 GACACTTGCCCTTGTGTGGGATCACCAAGACTTACACATTCAGATTAAAATGAACATCCAAGCAG 1171

Db   1032 GACACTGCCCTTGTGGGCCTCACCAAGACTTACACATTCAGGTTAAATGAGCAACTTCACAGC 1091
          |||||||||||||||||||||||||||||||||||
Qy   1172 TAAATTGGAGCCCCCCAGCTAAGTTACTTTGAGTATCGGAGGGGGTTACTCGCGGAACCTCACAGC 1231

Db   1092 TAATTGGAGCCCCCAGCTGAGTTACTTTGAGTATCGGAGGGGTTACTCGGGAACTCACAGC 1151
          |||||||||||||||||||||||||||||||||||
Qy   1232 CCTGCGGATCCGGAGCTACCTACGGAGAATACGTACTACTGGGTACATTGACAACGTGACCTT 1291

Db   1152 CCTCCGCATCCGAGCTACATATGGAGAATACAGTACTGGGTACATTGACAATGTGCCC 1211
          |||||||||||||||||||||||||||||||||||
Qy   1292 GATTTCAGCCGCCGCCCGTTTCTCGGAGCCCCCAGCCCGGGGTTGAACAGTGTATGTCC 1351

Db   1212 GATTTCAGCCGCGCCCGTTGCTCTGGAGCCCCAGCACCCTGGGGTTGAACAGTGTATGTCC 1271
          |||||||||||||||||||||||||||||||||||
Qy   1352 TGTTGGCTACAAGGGGCAGCAGTTCTGCCGGATTGTGCTTCCGGGTCTACAAGGAGATTCAGC 1411

Db   1272 TGTTGGGTACAAGGGGCAATTCCACCAAGGATTGTGCTTCTCTGGGTCTACAGGGAGATTCAGC 1331
          |||||||||||||||||||||||||||||||||||
Qy   1412 CAGACTGGGGACTTTTGGCACCTGTATTCCATTGTAACTACGGAGGGGGAGGGGCGCGA 1471

Db   1332 GAGACTGGGGGCCTTTTGGGCACCTGTATTCCTTGTAACTGTGTTCAAGGGAGGGGGCTGCGA 1391
          |||||||||||||||||||||||||||||||||||
Qy   1472 TCCAGACACAGGAGGACTGTTACTCAGGGGGATGAGAAACCTGACTCCCTGAGTTGTCCGA 1531

Db   1392 TCCAGACACAGGAGATTGTTATTCAAGGGGATGAGAATCCTGACAT---TGAGGTGTGCTGA 1448
          |||||||||||||||||||||||||||||||||||
Qy   1532 CTGCCCCAATTGGTTTGCCTCCGGTGATGCCTGAGCAGCAGCCGGGCCAAGCCGTGCCCCTG 1591

Db   1449 CTGCCCAATTGGTTTCTACAACGATCCCGAAGGACCCCGCCAGCTGCAAGCCGTGCCCCTG 1508
          |||||||||||||||||||||||||||||||||||
Qy   1592 TCGGCAATGGGTTCAGCTGTTCAGCTGCTCCGGTGATGCTCGAGCAGGTGGTGCAATAACTG 1651

Db   1509 TCATAACGGGTTCAGCTGCTTCACAACGATCCGGAGACACGGTGGTGTCCAATAACTG 1568
          |||||||||||||||||||||||||||||||||||
Qy   1652 CCCCCAGGTGTCACTGGTGCCCGGTGCTGTGAGCTCTGTTGCTGGACCC 1711

Db   1569 CCCTCCCGGGTCACCGGTGCCCGGTGCTGTGAGCTCTGTTGCTGGACCC 1628
          |||||||||||||||||||||||||||||||||||
Qy   1712 CTTCGGGGGAACGGTGGGCCCAGGCCTGTTGTCAGTGCGAACCAACGTGGA 1771

Db   1629 CTTTGGTGGAACATGGGCCCAGTGAGGGCTTTGCTCAGTGCAATGTGGA 1688
          |||||||||||||||||||||||||||||||||||
Qy   1772 CCCCTAGTTGCCTCCGGGAACTGTGACCGGCCTGACGAGGCAGGTGTCTGAAGTGCATCCACAA 1831

Db   1689 CCCCAGTGCCTCTGGGAATTGACCCGGCTGACGAGGCAGGTGTTTGAAGTGTTATCCACACAA 1748
          |||||||||||||||||||||||||||||||||||
Qy   1832 CACAGCCCGGGCATCTACTGCGACCAGTGCAAAGCAGGCTACTTCGGGACCCCAGTGGGCTCC 1891

Db   1749 CACAGCCGGGCATCTACTGCGACCAGTGCAAAGCAGGCTACTTCGGGACCCCAGTGGGCTCC 1808
          |||||||||||||||||||||||||||||||||||
Qy   1892 CAATCCAGCAGACAAGAGTCGGAGCTTGCAACCCAGTGGGGTCGGAGCCTGTGGA 1951

Db   1808 CAATCCAGCAGACAAGAGTCGGAGCTTGCAACCCAGTGGGGTCGGAGCCTGTGGA 1863
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Db  1809 CAACCCAGCAGACAAGTGTTGCGAGCTTGCAACTGTAACCCCATGGGGCTCAGAGCCTGTAGG 1868
Qy  1952 GTGTCGGAAGTGATGGCAGCTGTGTTTGGTGTGGCCTCAGCTGTGAGCA             2011
Db  1869 ATGTCGGAAGTGATGGCAGCCACCTGTGTTGTTTGCAAGCCAGGATTTCGGTGGGCCCAAACTGTGAGCA 1928

Qy  2012 TGCGCGCCACTGACCAGCTGTCCAGCTTGCTATAATCAAGTGAAGGTTCAGATGGATCAGTT       2071
Db  1929 TGGGAGCATT---CAGCTGTCCAGCTTGCTATAATCAAGTGAAGGATTCAGATGGATCAGTT      1985

Qy  2072 TATGCAGCAGCTCCAGATCCTCTGGAGGCCCTGATTTCGAAGGCTCAGG------TGGAGC     2125
Db  1986 TATGGCAGCAGCTTCAGAGAATGGAGGCCCCTGATTTCAAAGGCTCAGGGTGGTGGATGGAGT 2045

Qy  2126 AGTACCCACCACGACAGAGGCTGAAAGGCAGGAGGATGCAGCAGCAGGAGCAGCAT         2185
Db  2046 AGTACCCTGATACAGAGACTGGAAGGCAGGAGGATGCAGCAGCAGCAGCAGCCCCTTCAGGACAT 2105

Qy  2186 TCTGAGAAGAGCCCAGATTTCACAAGATGCTGTTAGATCCTTCAAATCTCCGGGTGCCAA      2245
Db  2106 TCTGAGAGATGCCCAGATTTCAAGAGGTGCTAGCAGATCCCTTGGTCTCCAGTTGGCCAA      2165

Qy  2246 GGCAAGGACTCAAGAGAAATAGCTACCGGGACCGCGCCTGGATGAGCTTAAGATGACTGTGGA   2305
Db  2166 GGTGAGGAGGCCAAGAGAACAGCTACCACAGAGCCGCGTCGGATGAGACCTCAAGATGACTGTGGA 2225

Qy  2306 AAGAGTTCGGGCCCTGGGGCAGCAGTCAGTATCAGAACCAAGTTCAGCAGGCTCAT          2365
Db  2226 AAGAGTTCGGGCCTCTGGGAGTCAGTACCAGAACCGAGTTCGGGGATTACTCACAGGCTCAT    2285

Qy  2366 CACTCAGATGCGCCTGAGCCGCTGGAGGAAAAGTGAGGGTTTCCCTGCAAAAACACCAACATTCC 2425
Db  2286 CACTCAGATGCGCCTGAGCCGCTGGAGGAAAGTGAAGCTTCCTTGGGAAAACACTAACANTTCC 2345

Qy  2426 TCCTTCAGAGCACTACGTGGGCGGGGCCAAATGGCTTTAAAAGTCTGGGCTTCAGGAGGCCCACGAG 2485
Db  2346 TGCCTCAGACACCACTACGTGGGGGCCAAATGGCTTTAAAAGTCTGGGCTTCAGGAGGCCCACAAG 2405

Qy  2486 ATTGGCAGACAGCAGCCATGTTCAGTCAGCTAACAGTGGCAAAGGAAAACCCA              2545
Db  2406 ATTAGCAGAAAGCCACAGTTGGAGTCAGCGACGCCACTGAACACGACAAGGGAAACTGA        2465

Qy  2546 GGAGTATTCCAAAAGAGCTGATGTCACTCGGTGGTGCGCGGGGCCTCTGCAGGAAGGGAG----- 2599
Db  2466 GGACTATTCCAAAACAAGCCCTCTCACTCGGTGGTGCCAAGGCCCCTGCAGGAGTCCGGAAG  2525

Qy  2600 CGGAAGCGGCGCAGCCTCGGACGGACGCCGGTGGTGCAAAGGCTTGTGTGGGAAAATGCAGAAAC  2659
Db  2526 CGGAAGCGGTTAGCCCCGGACCGGTGCTGTGGTGCAAGGGCTTGTGGGAAAATTGGGAGAAAAC 2585

Qy  2660 TAAATCTTGGCCCAGGAGTTGTCGAGGGAGGCCACGCAAACCGACATGGAAGGCAGATAG       2719
Db  2586 CAAGTCCCTGGCCCACTCAGTTGACAAGGGAGGCCCACTCAAAGCGGAAAATTGAAGCAGAATAG 2645

Qy  2720 GTCTTATCAGCATAGTCTCCACCCTTCTCAATTCCCTGTCTGTCTCAGATTCAGGGAGTCAATGA 2779
Db  2646 GTCTTATCAGCACACAGTCTCCCCCTCCTGGATTCAGTGTCTCCGCTTCAGGGGAGTCAGTGA  2705

Qy  2780 TCAGTCCCTTGCCAGGT----AGAAGCGAAGAGGGCTCAGACAAAAGAAAGCTGATTCTCTCAAA 2836
Db  2706 TCAGTCCCTTTCAGGTGGGAAGAAGCAAAAGAGGATCAAACAAAAGCGGGATTCAGTTCACTCTCAAG 2765

Qy  2837 CCGTTGTGACTTAAGCATATGGATGGATGAGTTCAAGCACGTGCAAAGCAAATCTGGGAAACTGGGA 2896
Db  2766 CCTCGTTAACCAGGCATATGGATGTNGAGTTCAAGCGGTACACAAAAAGAATTCTGGGAAACTGGAA 2825

Qy  2897 AGAAGAAAACCCGGCAGCAGCTCTTACACGAAATGGAAGACAGAGACACATCAGATCAGCT      2956
Db  2826 AGAAGAAGCACACAGCACCTCTTACAGAATGGGAAAAAGTGGGACGAGAAATCAGATCAGCT     2885

Qy  2957 GCTTTCCCGTGCCAACACTTTGCTAAAAGCACGAGCCCAAGAGGAGCACTAAGGTATATGGGCAAATGC 3016
Db  2886 GCTTTCCCCTGCCAAATCTTCCTAAAAGCACAAGAAGCACACTGAGTAGTATGGGCAAATGC     2945

Qy  3017 CACTTTTTATGAAGTTCAGACATCTTAAAGAATCTCAGAGAGTTTGACCTTGCAGGGTTGG     3076
Db  2946 CACTTTTTATGAAGTTGAGAGAGCCAATCCTTAAAAACCTCAGAGAGTTTGACCTGCAGGGTTGGA 3005

Qy  3077 AGATAAAAGAGCGAGAAGATCTGAAGAGCCATGGAGAGGGCCATGAGAGAGAGACTCTCCTACATCAGCAGCAGAAGGT 3136
Db  3006 CAAACAGAAAAGCAGAAGCTGAAGAAGCCATGAAGAGGCCATGAGAGAGACTCTCCTACATCAGCCAGAAGGT 3065

Qy  3137 TGCAGGTGCCAGTGACAAGACAGGAAGCAAAGCAGAAGCAGCCCTTGGGCAGTGTGCTCGTGCCGA 3196
Db  3066 TTCAGATGCCAGTGACAAGACCCAGCCAGCGGAAAAAGCCCCTGGGCAGCCCTGCTGGA        3125

Qy  3197 CGCCCAGAGGCGAAAGAATGCAGCCGACCCCGGGGAGGCGCCTGGGAGATCTCTGGCCAAGATAGAACA 3256
Db  3126 TGCACAGAGGCGCAAAGAATGGGGCGCCGAGGCCCCGGAAATCTCAGTGAGATTGAACA        3185

Qy  3257 GGAGATAGGGAGGTCTGAACTTGGAGGTGAAGCCAATGTGACAGCAGAGGGAGCCTTGGCCATGGA 3316
Db  3186 GGAGATTGGGAGTCTGAACTTGGAGGTGAAGCCAATGTGACAGCAGATGGGGCCTTGGCCATGGA 3245

Qy  3317 GAAAGGGACTGGCCACTCTGAAAAGTGAGATGAGATGAGAAGAGATGGAAAAGGTGAAGGAGGAA 3376
Db  3246 AAAGGGACTGGCGCCTCTCTGAAAGGTGAGGTGAAGCTGAGGAAGGAGGAA               3305

Qy  3377 GGAGCAGGAGAGTTTGACATGGATATGGACAGGTGCAGATGGTGGTTAATTGCAGAGGCCCAAAG 3436
Db  3306 GGAGCTGGAGTTTGACACGGATATGGATGCAGTACAGATGGTGGTTACAGGAGCCCCAGAA     3365

Qy  3437 AGTTGAAAACAGAGCCAAGAAATGCTGGAGTTACGATCCAAGGACACACTCAACACATTGGA    3496
Db  3366 GGTTGATACCAGAGCCAAGAAACTTGGAGTTACGATCCAAGAACACACTCAACACAATTAGA    3425

Qy  3497 TGGCATCCTACACCTAAATAGACCAGCCCTGGGCAGTGTGGGGATGAAGAGAGGGCTTCTTACT 3556
Db  3426 CGGCCTCCTGCATCTGATGGCACCAGCCCTCTCAGTGTGTAGATGAGAAGAACATTGTCTACT   3485

Qy  3557 GGAGCAGAAGCAGTTTTCCGAGTCCGAGCCCAAGACTCAGATCAACAGCAGCTCAGGGCCCCTGATGTC 3616
Db  3486 GGAGCAGAAAGCTTCCCGAGCCAAGATCAACCAGCCCAACAGCAACTACAGGGCCCCATAGTGTC 3545

Qy  3617 AGAGCTGGAAGAGAGGGAGCACATCGGCAGAAGGGCCAGAAGGGCCACCTCCGTTTCCTGGAGACTACCAT 3676
Db  3546 AGAGCTGGAAGAGAGGGCACGTCAGCGAGAGGGGCCACCTCCATTTGCTGGAGACAAAGCAT    3605

Qy  3677 AGATGGGGATTCTGGGTGTGATGTGAAGAAACCTGGAGAACATCAGGGACAACATCCTGGAGACAAAGC 3737
Db  3606 AGATGGGGATTCTGGCTGATGTGTGAAGAAAACCTTGGAGGCCAATTAGGACATCAGGGACATCAGGG 3665

Qy  3737 CTGCCTACAATACCCAGGCTCTTGAGCAAACAGTGACGAAGTGCCTTAGAGATTTTCTCAACCAA 3796
Db  3666 CTGCTACAATACCCAGGCTCTTGAGCAAACAGTGACGAAGCTGCCATAAATATTTCTCAACTGA 3725

Qy  3797 GGTTCTTGGGATTCAGACCTAGCTGCCTTAGAGATTTCTCA                         3837
Db  3726 GGTTCTTGGGATTACAGAATCTCAGGGGGCTCGGGAGCCCATGTCA                    3766
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